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SET3p monomethylates histone H3 on lysine 9 and is required for the silencing of tandemly repeated transgenes in *Chlamydomonas*

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ABSTRACT

SET domain-containing proteins of the SU(VAR)3-9 class are major regulators of heterochromatin in several eukaryotes, including mammals, insects, plants and fungi. The function of these polypeptides is mediated, at least in part, by their ability to methylate histone H3 on lysine 9 (H3K9). Indeed, mutants defective in SU(VAR)3-9 proteins have implicated di- and/or trimethyl H3K9 in the formation and/or maintenance of heterochromatin across the eukaryotic spectrum. Yet, the biological significance of monomethyl H3K9 has remained unclear because of the lack of mutants exclusively defective in this modification. Interestingly, a SU(VAR)3-9 homolog in the unicellular green alga *Chlamydomonas reinhardtii*, SET3p, functions *in vitro* as a specific H3K9 monomethyltransferase. RNAi-mediated suppression of *SET3* reactivated the expression of repetitive transgenic arrays and reduced global monomethyl H3K9 levels. Moreover, chromatin immunoprecipitation (ChIP) assays demonstrated that transgene reactivation correlated with the partial loss of monomethyl H3K9 from their chromatin. In contrast, the levels of trimethyl H3K9 or the repression of euchromatic sequences were not affected by *SET3* down-regulation; whereas dimethyl H3K9 was undetectable in *Chlamydomonas*. Thus, our observations are consistent with a role for monomethyl H3K9 as an epigenetic mark of repressed chromatin and raise questions as to the functional distinctiveness of different H3K9 methylation states.

INTRODUCTION

Transcriptional gene expression in eukaryotes is regulated at two major levels: the operation of the transcription machinery and the modulation of chromatin structure (1). Indeed, the regulation of chromatin packaging has recently emerged as an important mechanism for maintaining gene expression patterns. Eukaryotic genomes are commonly organized into two main types of chromatin: euchromatin, consisting of transcriptionally permissive or active domains, and heterochromatin, characterized by densely packed silent regions (2). These functionally and structurally distinct chromatin states are marked by distinctive covalent modifications on the DNA and on the nucleosomal histones. For instance, active euchromatin is usually characterized by the presence of histone H3 methylated on lysines 4 and 36; whereas silenced heterochromatin is often distinguished by the presence of histone H3 methylated on lysines 9 and 27, and histone H4 methylated on lysine 20 (3,4). This organization of chromosomes into domains with distinct histone methylation patterns appears to be common across the eukaryotic spectrum (5–12) and the histone modifications are proposed to influence directly chromatin structure and/or bring about the recruitment of chromatin modulators (3,4). However, it is becoming apparent that the specific modifications associated with functionally equivalent regions (such as pericentric heterochromatin) can be quite variable among different species.

Histone H3 on lysine 9 (H3K9) methylation is carried out by the SET domain of the SU(VAR)3–9-related proteins, which belong to the histone methyltransferase (HMTase) superfamily (13,14). The first SU(VAR)3-9-encoding gene was identified in a genetic screen for suppressors of position effect variegation in *Drosophila melanogaster* (15), providing clues as to its function as a key regulator of repressive heterochromatic organization. Indeed, *Drosophila* SU(VAR)3-9 and its mammalian homologs, SUV39H1 and SUV39H2, were latter found to be enriched in interphase heterochromatin and to accumulate transiently at centromeric loci during mitosis (16–18). SU(VAR)3-9-related proteins are now known to be widely distributed among eukaryotes. For instance, the model plant *Arabidopsis thaliana* contains 29 genes encoding SET domain proteins (19). Ten of these polypeptides have been classified as SU(VAR)3-9

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homologs (SUVHs), based on the degree of similarity between their SET domains and those of animal SU(VAR)3-9 proteins. *SUVH* genes have also been identified in a number of other plant species such as tobacco (20), maize (21) and rice (http://www.chromdb.org) as well as in several fungi (22,23). However, they have not been described as yet in algal systems.

Seven plant *SUVH* genes have been characterized in some detail: tobacco *NtSET1* (20,24,25), and *Arabidopsis SUVH1* (8), *SUVH2* (8), *SUVH3* (26), *SUVH4* (*KRYPTONITE*) (27,28), *SUVH5* (29) and *SUVH6* (30,31). Several of the corresponding proteins have been shown to possess HMTase activity targeting H3K9 (and H4K20 or H2A in the cases of SUVH2 and SUVH5, respectively) and to associate preferentially with putative heterochromatic regions (8,24,29). Indeed, *SUVH2* appears to play a major role in heterochromatin formation and/or maintenance in *Arabidopsis* since loss-of-function mutants display defects in gene silencing and a reduction in multiple heterochromatin-specific histone methylation marks (8). In contrast, *SUVH4*, *SUVH5* and *SUVH6* seem to have partly overlapping functions and control H3K9 methylation and gene silencing at specific loci (29,31).

Methylatable lysine residues can exist in monomethylated, dimethylated or trimethylated states, increasing the coding potential of modified histone lysines as epigenetic marks (4). Interestingly, in mammals, pericentric heterochromatin is enriched in trimethyl H3K9 (H3K9me3), a modification carried out predominantly by the SUV39H1 and SUV39H2 HMTases (4–6,9). Conversely, mono- and dimethyl H3K9 (H3K9me1 and H3K9me2) are enriched in certain euchromatic domains, which have been postulated to be transcriptionally silent (4–6,9,32). The latter modifications are mediated in part by the G9a HMTase, which plays an essential role in developmental regulation of gene expression (5,6,9,33). In *Arabidopsis*, in contrast to mammals, heterochromatic chromocenters are marked by H3K9me1 and H3K9me2, whereas H3K9me3 is predominantly found in euchromatic regions (7,8,27). Yet in another plant species, maize, only H3K9me1 was observed in heterochromatic domains (as well as in some euchromatic regions) while H3K9me2 and H3K9me3 were restricted to euchromatin and the centromeres (11).

These observations suggest that H3K9 mono-, di- and trimethylation states may serve distinct functions since they reside at least partly in separate chromosomal domains. Moreover, in mammals and *Arabidopsis*, different HMTases are responsible for specific degrees of H3K9 methylation at certain locations (5,6,9,29,34) and different HMTase mutants have distinct phenotypes (5,33), implying that the HMTases (and the histone modifications that they catalyze) are differentially targeted to diverse genomic regions for regulatory purposes. Yet, seemingly equivalent domains (such as pericentric heterochromatin) are characterized by species-specific H3K9 methylation states, raising questions as to the functional significance of different degrees of H3K9 methylation. In addition, genetic and biochemical analyses in a variety of eukaryotes have established a role for H3K9me2 and H3K9me3 in the formation and/or maintenance of transcriptionally repressive chromatin (3,4,8), whereas H3K9me1 lacks a defined functional assignment at present, partly because a HMTase exclusively responsible for this modification has not been identified thus far.

To gain further insight into the role of H3K9 methylation in chromatin organization, we undertook a reverse genetics approach to the study of SUVHs in the green alga *Chlamydomonas reinhardtii*. BLAST searches of the almost fully sequenced genome (http://genome.jgi-psf.org/Chlre3/Chlre3.home.html) revealed the existence of two SU(VAR)3-9-related proteins in *Chlamydomonas*. We report here on the characterization of one of these homologs, named SET3p. This polypeptide showed the same domain organization as plant SUVH proteins and its suppression by RNA interference (RNAi) released the transcriptional silencing of tandem transgenes. In contrast, repressed single-copy euchromatic sequences and dispersed transposons were not reactivated. Recombinant SET3p behaved, *in vitro*, as an exclusive monomethyl H3K9 HMTase. Moreover, chromatin immunoprecipitation (ChIP) assays demonstrated that, *in vivo*, H3K9me1 was dependent on the SET3p activity and was associated with silent multiple-copy transgenes. Conversely, H3K9me3 was mainly detected in a euchromatic gene and its intensity was not altered by *SET3* suppression. Thus, our results provide direct evidence for a functional role of monomethyl H3K9 in the maintenance of repressed chromatin and add to the growing body of evidence suggesting that seemingly equivalent chromatin states may be characterized by species-specific combinations of histone modifications.

MATERIALS AND METHODS

Chlamydomonas reinhardtii strains and culture conditions

Chlamydomonas cells were routinely grown in Tris-acetate-phosphate (TAP) medium under moderate light conditions (35,36). The 1-P[300] strain, containing over 100 integrated copies of the *RbcS2:aadA:RbcS2* transgene, has been previously described (35). The Set3-IR and Maa7-IR strains are derivatives of 1-P[300] in which the expression of *SET3* or *MAA7* (encoding tryptophan synthase β subunit) has been suppressed by RNAi, by using the approach described by Rohr *et al.* (37). Briefly, 1-P[300] was transformed by the glass bead method (35) with transgenes that produce double-stranded RNA (dsRNA) capable of inducing the degradation of homologous transcripts. For *SET3*, a 630-bp fragment corresponding to part of the coding sequence and the 3′ UTR of the transcript was amplified by PCR with primers Set3-F1 (5′-GCGACGGCAACCTGACCATCC-3′) and Set3-R1 (5′−CTGACCCCACACCCACGCTCTGAC-3′). This segment was then inserted in sense and antisense orientations, flanking a spacer sequence, in vector Maa7/X IR (37). The Maa7-IR3 construct, utilized as a negative control, has already been described (37). Reactivation of the *RbcS2:aadA:RbcS2* transgenes was tested by spotting serial dilutions of cells on TAP-agar plates with or without 50 mg/l of spectinomycin.

Reverse transcriptase-polymerase chain reaction (RT-PCR) analyses

Total RNA was isolated using the TRIZOL reagent, according to the manufacturer's instructions (Molecular Research Center, Cincinnati, OH, USA), and contaminant DNA was removed by DNase-I treatment (Ambion, Austin, TX, USA). First-strand cDNA synthesis and PCR reactions were performed as previously described by Rohr *et al.* (37). PCR products were resolved on 1.5% agarose gels and visualized by ethidium bromide staining. The numbers of cycles showing a linear relationship between input RNA and the final product were determined in preliminary experiments. Controls included the use as template of reactions without RT and verification of PCR products by hybridization with specific probes (data not shown). The primer sequences were as follows: for *SET3*, Set3-RTF6 (5′-GGTGTGC AAGTTCCTGATGCAC-3′) and Set3-RTR7 (5′-TGAA CTGCAGCATCTCCTCGTC-3′); for *aadA*, aadA-CodL, (5′-TCTGGCTATCTTGCTGACAAAA-3′); and aadA-CodR, (5′-TAGTGATCTCGCCTTTCACGTA-3′); and for *MUT9*, Mut9-5 (5′-GCTGTACATCTCGTGCGTGT-3′) and Mut9-2 (5′-ATGGCGGTCACGTAGAAGC-3′).

Phylogenetic analysis

Individual domains present in SET3p (AAV84356) and other SU(VAR)3-9-related proteins were identified using the SMART database (38). The SET domain amino acid sequences were aligned using CLUSTAL X version 1.81 (39) and manually corrected with the GENEDOC program (http://www.psc.edu/biomed/genedoc). Phylogenetic relationships between these sequences were inferred by the neighbor-joining (NJ) method (40). The MEGA program version 3.1 (41) was used to obtain the NJ trees, using Poisson-corrected amino acid distances, and the bootstrap support values for 1000 pseudoreplicates.

Partial protein purification and immunoblotting

Chromatin-associated proteins were partially purified by differential centrifugation prior to immunoblotting. Approximately 5×10^8 TAP-grown cells were resuspended in nuclear isolation buffer (20 mM PIPES, pH 7.0, 0.25 M sucrose, 10 mM $MgCl_2$, 2.0 mM spermidine, 100 mM sodium butyrate, 0.1% Triton X-100, 5 mM β-mercaptoethanol, 2 mM benzamidine and 0.1 mM PMSF) and broken by two passages through a French press at 5000 psi. Lysed cells were then centrifuged for 10 min at 30 000 *g*. The supernatant was discarded and proteins in the pellet (including nuclear chromatin) were solubilized in high salt buffer (20 mM HEPES, pH 7.5, 2 M NaCl, 1 mM EDTA, 1 mM DTT, 2 mM benzamidine and 2 µl/ml of plant protease inhibitor cocktail [Sigma-Aldrich, Saint Louis. MO, USA]). Soluble proteins were then separated from insoluble debris by centrifugation for 10 min at 10 000 *g*, resolved by SDS-PAGE and transferred to nitrocellulose membranes. Specific methylated states of histone H3 lysine 9 were detected with antibodies against monomethyl H3K9 (Upstate, 07-395; or Abcam, ab9045), dimethyl H3K9 (Upstate, 07-212; or Abcam, ab7312) or trimethyl H3K9 (Abcam, ab1186 or ab8898). A modification-insensitive anti-H3 antibody (Abcam, ab1791) was used to adjust the amount of histone H3 loaded in each lane.

Histone methyltransferase assays

The histone methylating activity of recombinant SET3p was assayed as described earlier (42). Briefly, 10 µg of core histones or purified H3 from calf thymus and 1 µg of recombinant SET3p protein or a protein extract from an empty vector control were incubated with 250 nCi of S-adenosyl-L-(methyl-^{14}C)methionine (^{14}C-SAM) (GE Healthcare, Piscataway, NJ, USA) in a final volume of 40 µl for 2 h at 30°C in MAB buffer. Samples were then resolved by SDS-PAGE on 15% polyacrylamide gels, stained with Coomassie Brilliant Blue and dried onto filter paper. The incorporated radioactivity was detected with a phosphor imager (Amersham). The methylation activity of SET3p on wild-type (H3N) and lysine mutated (K4R, K9R, K27R or 3K-R) histone H3 tails fused to GST was assayed in a similar way. For time course experiments, 8 µg of recombinant SET3p protein, 40 µg of recombinant human histone H3 (43) and 20 µM of unlabeled SAM were incubated at 30°C in MAB buffer in a final volume of 80 µl. Ten microliters of aliquots were taken at different times (Figure 3D) and the reactions stopped by the addition of 10 µl of 2× SDS-PAGE loading buffer. Samples were then examined by western blotting with antibodies against specific H3K9 methylation states.

Chromatin immunoprecipitation (ChIP) assays

To examine the methylation status of histone H3 at specific chromosomal loci, 5×10^7 TAP-grown cells were cross-linked for 10 min with 1% formaldehyde and then quenched by adding glycine to 0.1 M. Cells were then pelleted, washed with TBS and frozen in liquid nitrogen (42). The cell pellet was resuspended in 6 ml of ChIP lysis buffer (20 mM Tris-HCl, pH 8.0, 150 mM NaCl, 1 mM EDTA, 0.1% SDS, 1% Triton X-100, 2 µl/ml of plant protease inhibitor cocktail [Sigma-Aldrich]), and cells were lysed by two passages through a French press at 5000 psi. Chromatin was sheared by sonication to an average size of 500 bp and then immunoprecipitated using a ChIP assay kit (Upstate) and a modification-insensitive anti-H3 antibody (15 µl, Abcam ab1791). The precipitated chromatin was eluted by incubation for 10 min at 68°C with 100 µl of ChIP elution buffer (50 mM Tris-HCl, pH 7.5, 10 mM EDTA and 1% SDS) (44). This procedure was repeated once and 10% of the combined eluate was removed to be used as the H3 secondary input (see reference 44 for a justification). The remaining eluate was diluted to 2 ml with ChIP lysis buffer containing 25 µg/ml of sheared salmon testes DNA (Sigma-Aldrich), and 5 mg/ml BSA (Fraction V, Sigma-Aldrich); and then the chromatin was immunoprecipitated with a second antibody against monomethyl H3K9 (15 µl, Upstate, 07-395), trimethyl H3K9 (3 µg, Abcam ab1186) or rabbit IgG (5 µl at 2 µg/µl Sigma-Aldrich, I5006). After cross-link reversal and DNA purification by phenol/chloroform

extractions, the immunoprecipitated DNA was quantified by real-time PCR on a Bio-Rad iCycler iQ using SYBR Green. After each run, a melting curve was performed to ensure that no primer dimers interfered with the quantification. Serial dilutions of the primary input (DNA prior to anti-H3 immunoprecipitation) were used to generate a calibration curve with which the amounts of target DNA in the secondary inputs (DNA co-immunoprecipitated with anti-H3, anti-H3K9me1, anti-H3K9me3 or IgG antibodies) were calculated. The levels of the H3K9 modifications or of the IgG negative control were then normalized relative to the anti-H3 controls for each examined sequence. Primers used for amplification of the target loci were: for *RbcS2:aadA:RbcS2*, aadA-CodL (5′-TCTGGCTATCTTGCTGACAAAA-3′) and aadA-CodR (5′-TAGTGATCTCGCCTTTCACGTA-3′); and for *RPS3*, C_20102proL1 (5′-AAGGGCGCTGCTAGTATAACCA-3′) and C_20102proR1 (5′-CCTTTGTTCCCGAGAGAGAGAA-3′).

DNA methylation analysis

Genomic DNA from *Chlamydomonas* was isolated, digested, resolved in agarose gels, blotted and hybridized following standard procedures (35,45). The *aadA* and *psbA* probes used for Southern hybridization correspond to the coding sequence of the *RbcS2:aadA:RbcS2* transgene and the 3′ end of the chloroplast *psbA* gene, respectively (35).

RESULTS

Chlamydomonas reinhardtii SET3p is a homolog of plant SUVH proteins

SET3 encodes a SET domain-containing protein with a predicted size of 957 amino acids. The carboxyl terminal region of this polypeptide is well conserved relative to that of SU(VAR)3-9 proteins and consists of the SET domain flanked by two cysteine-rich motifs, the pre-SET and the post-SET domains (Figure 1A). However, SET3p also includes a unique insertion, of approximately 300 amino acids, within the SET domain that separates the conserved sub-motifs II and III (46) (Figure 1A). At its N-terminal end, SET3p displays the configuration characteristic of plant SUVH proteins (Figure 1A).

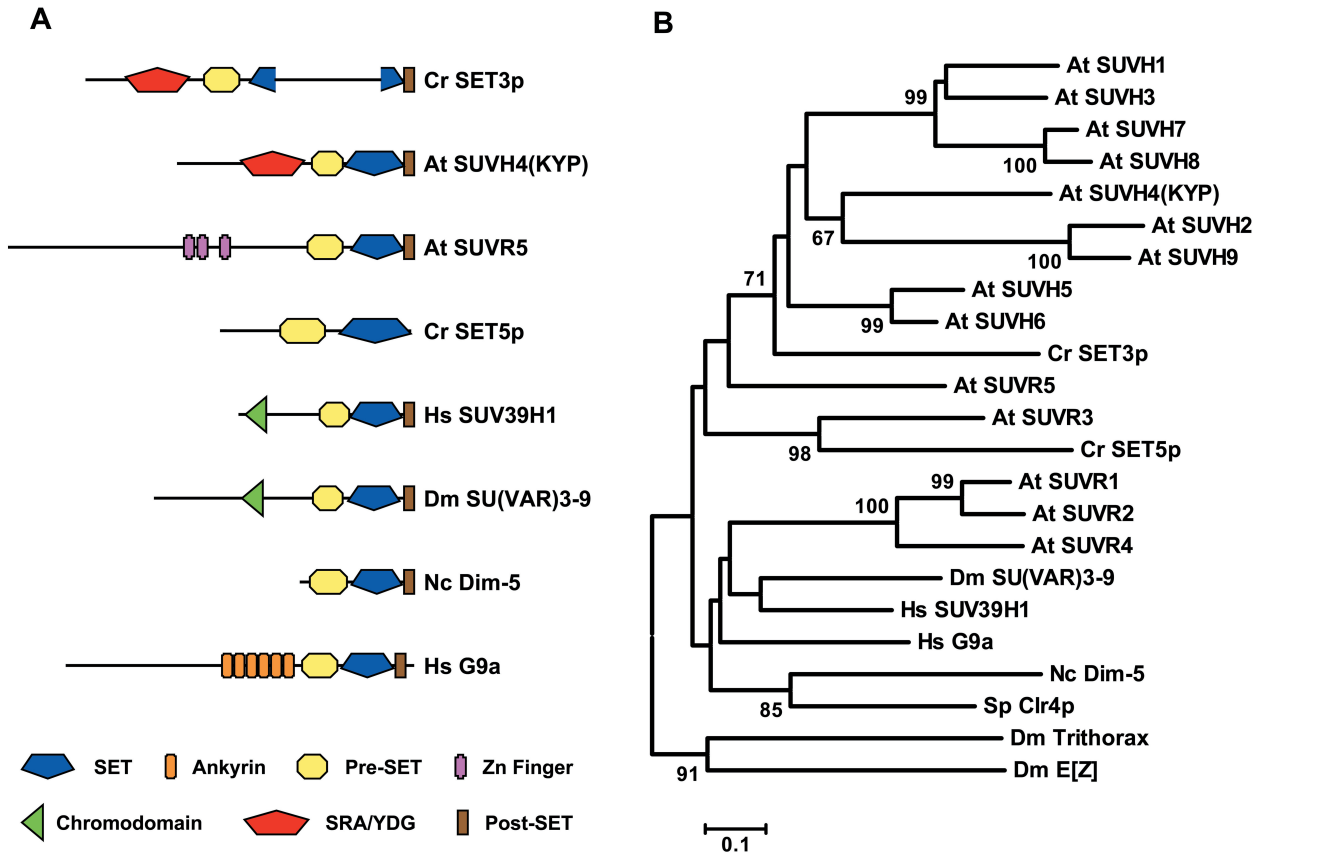

Figure 1. SU(VAR)3-9 homologs in *Chlamydomonas* and several eukaryotes. (**A**) Domain organization of SU(VAR)3-9-related proteins. (**B**) Phylogenetic relationship between *Chlamydomonas* SET3p and SET5p and histone methyltransferases from several species. Numbers indicate bootstrap values, as percentage, based on 1000 pseudoreplicates. At SUVH1 to At SUVH9, *Arabidopsis thaliana* SU(VAR)3-9 homologs 1 to 9 (AAK28966 to AAK28974, respectively); At SUVR1 to At SUVR5, *A. thaliana* SU(VAR)3-9-related 1 to 5 (AAK77165, AAK92218, NP_974212, AAL01113 and NP_179954, respectively); Cr SET3p, *Chlamydomonas reinhardtii* SET3p protein (AAV84356); Cr SET5p, *C. reinhardtii* SET5p protein (145254 at http://genome.jgi-psf.org/Chlre3/Chlre3.home.html); Dm E[Z], *Drosophila melanogaster* Enhancer of zeste protein (P42124); Dm SU(VAR)3-9, *Drosophila* Suppressor of variegation 3-9 protein (P45975); Dm Trithorax, *Drosophila* Trithorax protein (P20659); Hs G9a, human SET domain protein G9a (NP_006700); Hs SUV39H1, human SU(VAR)3-9 homolog 1 (O43463); Nc Dim-5, *Neurospora crassa* Dim-5 (Q8X225); Sp Clr4, *Schizosaccharomyces pombe* Cryptic loci regulator 4 protein (AAC18302).

These polypeptides contain, instead of the characteristic chromodomain of the metazoan enzymes, a conserved motif designated YDG or SRA (SET and RING finger associated) (19,47).

A phylogenetic tree constructed using sequences corresponding to the SET domain of multiple HMTases shows that SET3p clusters with the plant SUVH proteins (Figure 1B). These polypeptides have been reported to fall into four distinct subgroups, suggesting a possible functional differentiation that might have preceded the angiosperm/gymnosperm divergence (8,19,21). However, SET3p behaves as an outgroup to all of the *Arabidopsis* SUVH proteins, implying that most of the functional diversification of SUVH polypeptides likely occurred within the plant lineage after the evolutionary separation of green algae and land plants. In addition, higher plants also contain SU(VAR)3-9-RELATED (SUVR) proteins, which lack the YDG/SRA domain but are grouped with the SUVHs into the Class V of plant SET domain polypeptides (19,21). The *Chlamydomonas* genome also encodes a SU(VAR)3-9-related protein, named SET5p (145254 at http://genome.jgi-psf.org/Chlre3/Chlre3.home.html), that lacks the YDG/SRA domain (Figure 1A). Interestingly, whereas *Chlamydomonas* SET3p is closely related to plant SUVHs, SET5p associates with plant SUVRs in phylogenetic analyses (Figure 1B), suggesting that differentiation of the *SUVH* and *SUVR* genes likely occurred prior to the divergence of the green algae and plant lineages.

RNAi-mediated suppression of *SET3* results in defective silencing of multiple-copy transgenes

Plant *SUVH* genes have been implicated in gene silencing, heterochromatin formation and the partial control of non-CpG DNA methylation. For instance, *SUVH4* mutants derepress the silenced *SUPERMAN* and *PAI* genes (27,28) and loss-of-function of *SUVH2* reactivates a *LUCIFERASE* transgene (8). To examine whether *Chlamydomonas SET3* has a similar role in gene silencing, we tested the effect of downregulating its expression on the transcriptional activity of repressed transgenes. *Chlamydomonas* strain 1-P[300] contains over 100 silenced copies of the *RbcS2:aadA:RbcS2* transgene (conferring resistance to spectinomycin), integrated as head-to-head, tail-to-tail and head-to-tail concatamers at two chromosomal loci (35). Based on the repeated conformation of the transgenic arrays, their transcriptionally silenced state (35) and the presence of DNA methylation (see below), it is possible that the chromatin associated with these loci is (hetero)chromatic in nature, as reported for equivalent concatamers in other eukaryotes (8,48–50).

To suppress *SET3* expression, the 1-P[300] strain was transformed with an inverted repeat construct that generates dsRNA homologous to the 3′ end of the *SET3* mRNA. We recovered several independent transformants showing reduced *SET3* transcript levels and two strains, Set3-IR1 and Set3-IR2, were examined in detail for reactivation of the *RbcS2:aadA:RbcS2* transgenes as well as for their ability to survive on medium containing spectinomycin (Figure 2 and data not shown). RT-PCR analyses indicated that RNAi-mediated *SET3* suppression resulted in increased *RbcS2:aadA:RbcS2* mRNA levels (Figure 2A). In addition, the Set3-IR strains were able to grow on medium containing spectinomycin whereas the non-transgenic wild-type (CC-124) and the silenced parental strain (1-P[300]) were not (Figure 2B). These effects were specific for the Set3-IR transformants since RNAi-mediated downregulation of an unrelated gene, *MAA7* (encoding tryptophan synthase β subunit), did not reactivate *RbcS2:aadA:RbcS2* expression in the 1-P[300] strain nor allow survival in the presence of spectinomycin (Figure 2, Maa7-IR3 strain). Yet, *SET3* suppression did not release the silencing of an unmethylated, single-copy transgene (in strain 11-P[300]) or of dispersed transposable elements, such as the *TOC1* retrotransposon (data not shown). We have reported earlier that the 11-P[300] transgene and the *TOC1* loci appear to be repressed by euchromatin-specific epigenetic marks (42).

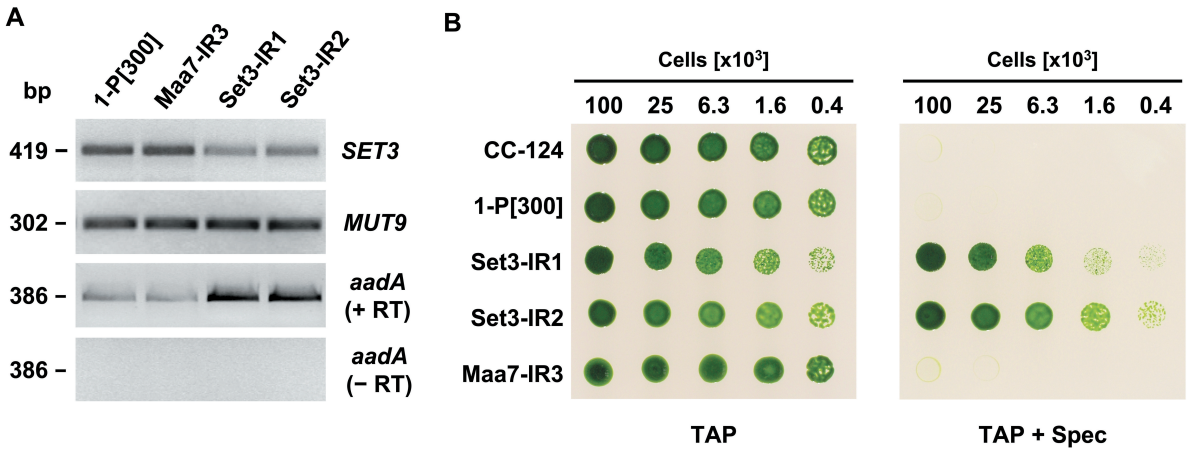

Figure 2. Suppression of *SET3* expression and reactivation of *RbcS2:aadA:RbcS2* transgenes in Set3-IR strains. (**A**) RT-PCR analysis of *SET3* and *RbcS2:aadA:RbcS2* (*aadA*) expression in the indicated strains. Amplification of *MUT9* (encoding a Ser/Thr protein kinase) transcripts was used as a control for equivalent RNA input and efficiency of the RT-PCR reactions. (**B**) Growth and survival of the indicated strains on medium with (TAP + Spec) or without (TAP) spectinomycin. Strains: CC-124, wild-type strain; 1-P[300], silenced parental strain; Maa7-IR3, 1-P[300] transformant expressing dsRNA complementary to the *MAA7* gene; Set3-IR1 and Set3-IR2, 1-P[300] transformants expressing dsRNA complementary to *SET3*.

Thus, our results suggest that downregulation of *SET3* expression leads to defects in the transcriptional silencing of multiple-copy *cis*-tandem transgenes, presumably associated with a (hetero)chromatic conformation (see discussion).

SET3p possesses H3K9 monomethyltransferase activity *in vitro*

In order to investigate whether SET3p might be a determinant of repressed chromatin structure, we first tested its ability to methylate core histones *in vitro*. Recombinant, His-tagged SET3p was purified from *Escherichia coli* and used in a methylation assay with a mix of calf thymus histones or purified histone H3 as the substrates. When SET3p was incubated with histones in the presence of ^{14}C-SAM, as the methyl donor, a 17-kDa band corresponding to methylated histone H3 was readily detected by phosphor imager scanning (Figure 3A). On the contrary, no signal was observed when core histones were incubated with an empty vector protein extract.

We next examined the histone H3 lysine residue that was targeted by the SET3p activity. We carried out *in vitro* HMTase assays using as substrates the histone H3 N-terminal tail (amino acids 1–52) with the wild-type sequence (H3N) or with mutations to arginine in specific lysines (K4R, K9R or K27R) or in the three lysine residues (3K-R = K4R, K9R and K27R). These polypeptides were expressed as GST fusions in *E. coli* and purified as recombinant proteins. When incubated in the presence of SET3p and ^{14}C-SAM, H3N was readily methylated, whereas recombinant GST alone did not serve as a substrate (Figure 3B, lanes 1 and 2). The K4R and K27R fusions, carrying mutations in H3 lysine 4 or 27, were methylated as well as H3N (Figure 3B, lanes 3 and 5). Conversely, mutation of H3 lysine 9 (K9R) or of the three lysine residues (3K-R) completely eliminated methylation by SET3p (Figure 3B, lanes 4 and 6). Thus, SET3p appears to have HMTase activity specific for lysine 9 of histone H3.

Several residues within the SET domain have been shown to be important for the degree of methylation carried out by an HMTase, with the Phe/Tyr switch being the most extensively characterized (51). The SET domains of proteins with di- and/or trimethylating activity generally posses a Phe residue, corresponding to positions 281 in *Neurospora crassa* Dim-5 and 943 in human G9a (Figure 3C). In contrast, a Tyr residue at this position inhibits trimethylation and Phe-to-Tyr mutants of both Dim-5 and G9a show altered specificity behaving as mono- or dimethyltransferases (51,52). SET3p contains a Tyr in the position corresponding to the Phe/Tyr switch (Figure 3C), suggesting that it might be restricted in its capacity to carry out trimethylation. To address this question, we incubated SET3p with recombinant

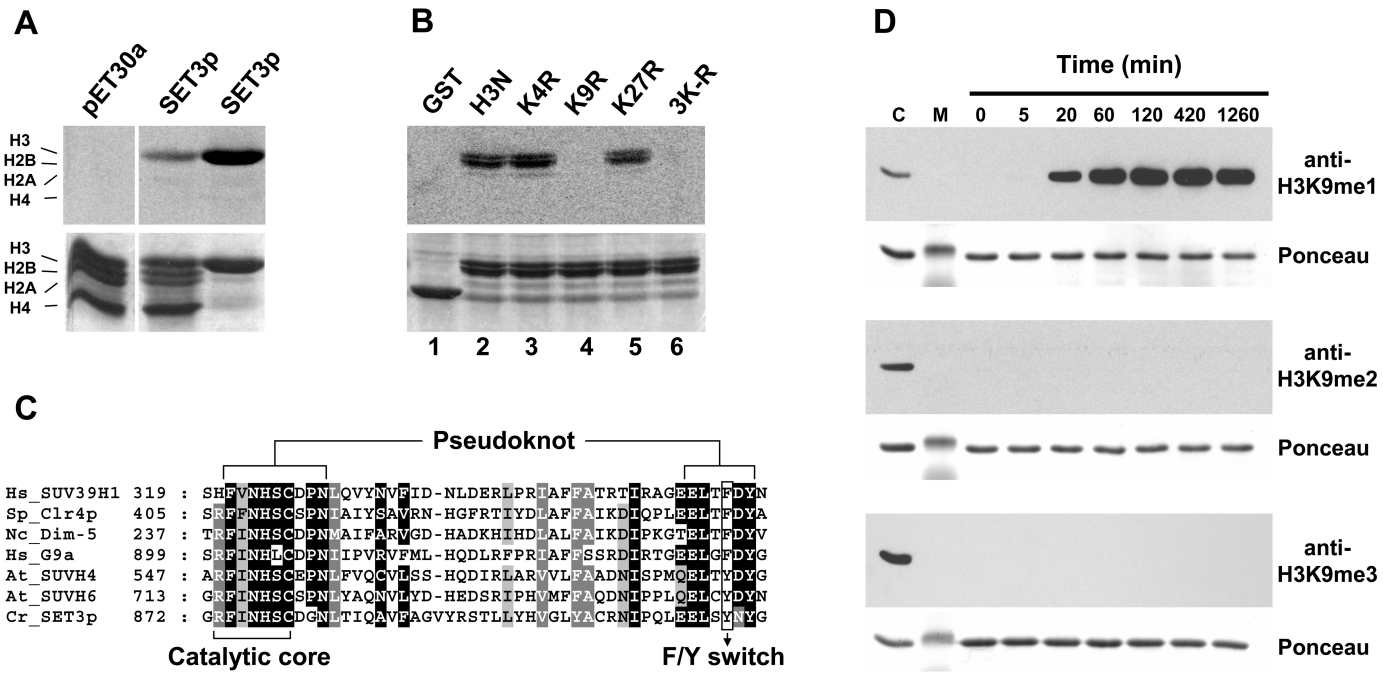

Figure 3. *In vitro* histone methyltransferase activity of recombinant SET3p. (**A**) His-tagged SET3p exclusively methylates histone H3. The recombinant protein was used in HMTase assays with calf thymus core histones or purified histone H3 as substrates. Samples were resolved by SDS-PAGE and stained with Coomassie blue (Bottom panel). Incorporation of the radiolabeled methyl group was detected by phosphor imaging (Top panel). pET30a indicates an empty vector protein extract used as a negative control. (**B**) HMTase assays of SET3p using as substrates wild-type and lysine mutants of the histone H3 N-tail fused to GST. Radiolabeled proteins were detected as in (**A**). Bands observed below the full-length substrates are likely degradation products. Bottom panel, Coomassie blue staining; Top panel, phosphor imager scan. (**C**) Alignment of the region corresponding to the pseudoknot in the SET domain of several SU(VAR)3-9 proteins. The position of the first amino acid in the alignment is indicated on the left. The Phe/Tyr (F/Y) switch, determining the degree of methylation by HMTases (51), is also shown. (**D**) SET3p specifically monomethylates H3K9 *in vitro*. Purified SET3p was incubated with recombinant human histone H3 in the presence of cold SAM for different amounts of time. Samples were resolved by SDS-PAGE, transferred to nitrocellulose and probed with the indicated antibodies. Equivalent loading of the lanes was checked by Ponceau S staining. C, purified calf thymus (non-recombinant) H3; M, molecular weight markers.

(unmethylated) histone H3 in the presence of unlabeled SAM and proceeded to detect the degree of SET3p-catalyzed H3K9 methylation by immunoblotting with antibodies raised specifically against mono-, di- or trimethyl H3K9. Interestingly, SET3p carried out mono-methylation of H3K9, which reached a plateau after 2–3 h of incubation (Figure 3D). In contrast, neither di- nor trimethylation of H3K9 could be detected, even after 21 h of incubation. These observations, taken together, indicated that SET3p behaves *in vitro* as an exclusive H3K9 monomethyltransferase.

SET3p is responsible for H3K9 monomethylation, but not H3K9 trimethylation, *in vivo*

Given its *in vitro* role as a H3K9 HMTase, we next examined whether SET3p affected this modification *in vivo*. Immunoblots of extracts enriched in chromatin proteins, probed with antibodies raised against the different forms of methylated H3K9, revealed the presence of H3K9me1 and H3K9me3 in *Chlamydomonas* (Figure 4A). In contrast, as reported earlier (42), dimethyl H3K9 was undetectable even though the anti-H3K9me2 antibody was capable of recognizing this modification in calf thymus histone H3 (Figure 3D, control). Interestingly, significantly lower levels of monomethyl H3K9 were observed in the strains undergoing suppression of *SET3* expression, whereas trimethyl H3K9 remained unchanged, in comparison with the parental 1-P[300] strain (Figure 4A). Global H3K9me1 and H3K9me3 levels in the control Maa7-IR3 strain were similar to those in the 1-P[300] strain (Figure 4A). Hence, in agreement with the *in vitro* data, *Chlamydomonas* SET3p seems to be at least partly responsible for global H3K9 monomethylation *in vivo*, whereas H3K9me3 depends on another yet unidentified HMTase.

Monomethyl H3K9 is associated with the chromatin of silenced, multiple-copy transgenes

To determine if the loss of H3K9me1 in the Set3-IR strains was directly associated with reactivation of the silenced *RbcS2:aadA:RbcS2* transgenes, we analyzed their chromatin environment by sequential ChIP assays. By using primers specific for the 5′ end of the coding sequence of the *RbcS2:aadA:RbcS2* transgene and real-time PCR, we found that monomethyl H3K9 was highly enriched in the silenced, multiple-copy transgenes (Figure 4B). In contrast, H3K9me1 was virtually absent from an equivalent region in the constitutively expressed *RPS3* gene (encoding ribosomal protein S3) (Figure 4B). ChIP analysis also revealed a substantial decrease in monomethyl H3K9 associated with the *RbcS2:aadA:RbcS2* transgenes in the Set3-IR2 strain, as compared with the parental 1-P[300] strain (Figure 4B). Unexpectedly, trimethyl H3K9 was almost undetectable in the *RbcS2:aadA:RbcS2* transgenes (independently of their transcriptional state), whereas low levels of H3K9me3 were observed in the transcriptionally active *RPS3* gene. Furthermore, no differences in H3K9me3 signals were discernable between the Set3-IR2 and the 1-P[300] strains at the tested loci. Thus, in

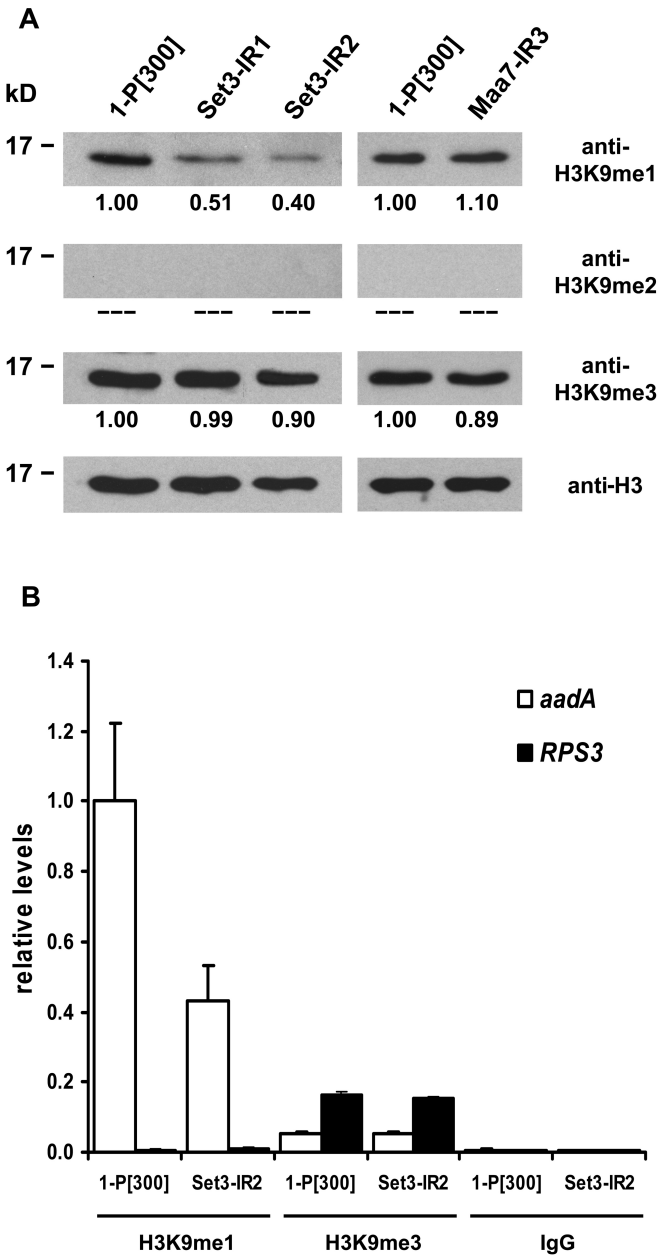

Figure 4. Monomethyl H3K9 is dependent on SET3p and is associated with the transcriptionally silenced *RbcS2:aadA:RbcS2* transgenes. (**A**) Immunoblot analysis of *in vivo* H3K9 methylation states. Partially purified chromatin proteins from the indicated strains were separated by SDS-PAGE, transferred to nitrocellulose and probed with antibodies raised against mono-, di- or trimethyl H3K9. Sample loading was calibrated based on immunoblots with an anti-H3, modification-insensitive antibody. Numbers below the panels indicate relative levels of a specific histone modification normalized to the histone H3 amount. (**B**) Association of mono- and trimethyl H3K9 with the silent *RbcS2:aadA:RbcS2* transgenes and the transcriptionally active *RPS3* gene. Sequential ChIP assays were performed on TAP-grown cells of the indicated strains using an antibody against histone H3, and then antibodies against monomethyl H3K9, trimethyl H3K9 or rabbit IgG (negative control). Immunoprecipitated DNA was examined by real-time PCR. For illustration purposes, enrichment was calculated relative to the anti-H3 co-immunoprecipitated DNA and then normalized to the level of monomethyl H3K9 associated with the *RbcS2:aadA:RbcS2* transgenes in the 1-P[300] strain. Results represent the mean ± SD of three independent experiments.

Chlamydomonas, monomethyl H3K9 may function as an epigenetic mark for the silenced chromatin, presumably heterochromatic-like, typical of tandem transgenes. Conversely, trimethyl H3K9 was not associated with the repressed *RbcS2:aadA:RbcS2* transgenes and the low levels detected on the active *RPS3* gene suggest that this modification may be present in euchromatic domains.

CpG DNA methylation of the *RbcS2:aadA:RbcS2* transgenes is increased in strains experiencing RNAi-mediated suppression of *SET3*

Since in some species cytosine methylation appears to be dependent on H3K9 methylation (4,23,27,29) and direct interaction between H3K9 HMTases and DNA methyltransferases has been demonstrated in mammals (53), we also studied the effect of *SET3* downregulation on the DNA methylation of the *RbcS2:aadA:RbcS2* transgenes. The methylation-sensitive isoschizomers HpaII and MspI recognize the same DNA sequence (5′-CCGG-3′), but HpaII is inhibited by methylation of either cytosine, whereas MspI is only sensitive to methylation of the outer cytosine residue. Thus, digestion of an unmethylated *RbcS2:aadA:RbcS2* transgene with these enzymes and HindIII generates a fragment of 530 bp and three fragments smaller than 160 bp that can be detected by hybridization with a probe encompassing the *aadA* coding sequence (Figure 5A). In contrast, if some of the HpaII/MspI sites become methylated, the inability of the enzymes to cleave will result in the appearance of DNA fragments of higher molecular weight. By using this approach, we observed that the multiple copies of the *RbcS2:aadA:RbcS2* transgene were nearly fully digested with MspI but only partly cleaved with HpaII in the 1-P[300] parental strain (Figure 5B), suggesting the presence of CpG DNA methylation in the *aadA* coding sequence and, possibly, in the upstream *RbcS2* promoter. The almost complete digestion with MspI indicated that CpNpG methylation (at least in a CCG context) is virtually absent from the *RbcS2:aadA:RbcS2* transgenes. Interestingly, in the Set3-IR strains we detected a noticeable decrease in the cleaving capability of HpaII, indicative of a higher degree of CpG DNA methylation in comparison to the 1-P[300] strain, whereas the patterns of MspI digestion remained unchanged (Figure 5B). As a control, Southern hybridization analysis of the same blots with a *psbA* (encoding a Photosystem II component) probe showed that the chloroplast DNA was equally digested in all lanes, substantiating that differences in *aadA* restriction patterns were not due to defective enzymatic activity in some samples. Similar results were observed with other methylation sensitive restriction enzymes, such as HhaI and ScrFI (data not shown). Thus, RNAi-mediated downregulation of *SET3* appears to result in increased levels of CpG DNA methylation associated with the *RbcS2:aadA:RbcS2* transgenes.

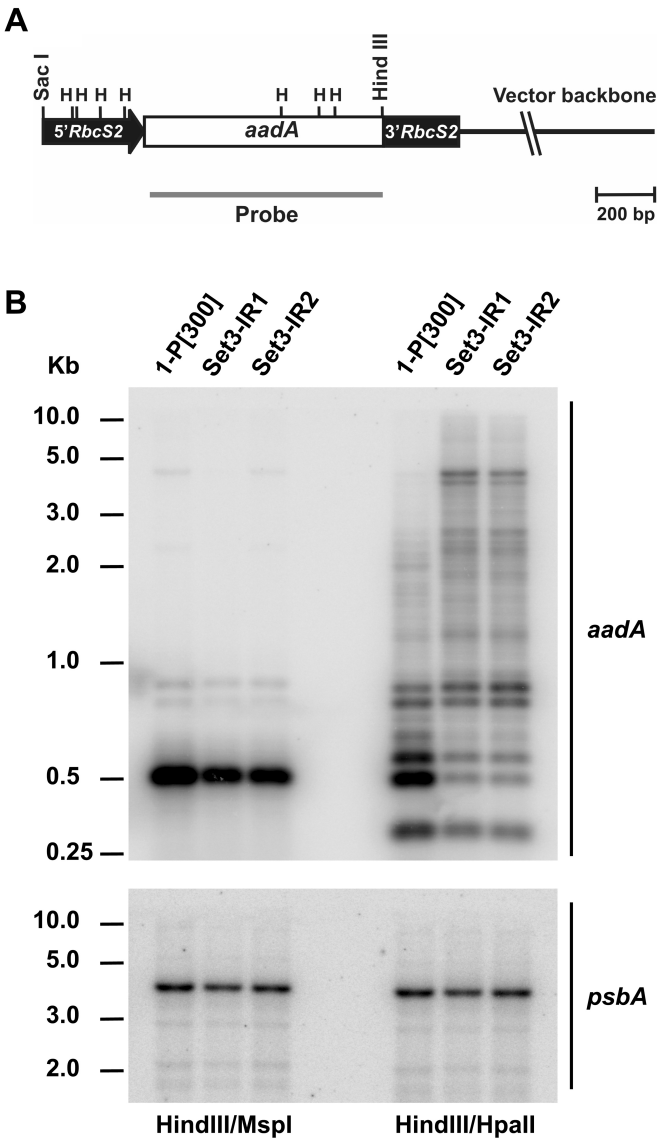

Figure 5. Effect of *SET3* suppression on the DNA methylation of the *RbcS2:aadA:RbcS2* transgenes. (**A**) Schematic representation of the plasmid containing the *RbcS2:aadA:RbcS2* transgene. The SacI restriction site, used to linearize the vector prior to transformation, and the probe used for Southern blot analyses are shown. H, HpaII/MspI restriction sites. (**B**) Total DNA of the indicated strains was digested with HindIII/MspI or HindIII/HpaII, separated by agarose gel electrophoresis, transferred to a nylon membrane and hybridized sequentially with probes corresponding to the *aadA* coding sequence (Top panel) or the 3′ end of the chloroplast *psbA* gene (Bottom panel). DNA size markers in kilobases are indicated on the left.

DISCUSSION

SUVHs are conserved proteins directly implicated in chromatin-mediated silencing in a variety of eukaryotes. Mammalian SUV39H1 and G9a act as transcriptional repressors in reporter-based transient expression assays (54,55) and fission yeast Clr4 is a key component in the silencing of transgenes integrated into heterochromatic regions (22). *Arabidopsis* mutants defective in *SUVH4* were repeatedly isolated as suppressors of silencing of certain alleles of the *SUPERMAN* and *PAI2* genes (27,28); and *SUVH2* was shown to affect the transcriptional repression of *LUCIFERASE* transgenic repeats in a dosage-dependent manner (8). Consistent with its relatedness to plant SUVH proteins, *Chlamydomonas* SET3p is

also involved in the transcriptional silencing of tandemly repeated transgenes. However, the expression of single-copy transgenes and dispersed endogenous transposons, previously shown to be repressed by euchromatic histone marks (42), was not affected by RNAi-mediated suppression of *SET3*. Although, we cannot rule out that partial downregulation of *SET3* may have not reduced the corresponding protein to a level low enough to compromise the silencing of euchromatic sequences. Nonetheless, in a number of species, transgenic repeat arrays appear to become silenced by condensation into heterochromatin (8,48,49,50), an intrinsic property of tandem arrays not attributable to position effects of nearby sequences (56,57). Indeed, it has been proposed that this form of repression may reflect a genomic defense response against invading foreign sequences such as transposable elements (56). Likewise, we speculate that concatameric transgenes in *Chlamydomonas* may be characterized by a (hetero)chromatic configuration that is at least partly dependent on SET3p activity. Although, the current lack of sequence data on heterochromatic *Chlamydomonas* repeats prevented us from testing more directly whether SET3p is required for the maintenance of natural heterochromatin.

The role of SU(VAR)3-9 proteins in the organization of transcriptionally repressive chromatin is mediated, at least in part, by their specific H3K9 methyltransferase activity (8,10,58). However, the ε-amino group of H3K9 can be mono-, di- or trimethylated, thereby adding to the coding complexity of this particular histone modification. In mammals, as already mentioned, pericentric heterochromatin is characterized by H3K9me3 and this modification is almost entirely eliminated in *suv39h1*/*suv39h2* double mutants, where H3K9me1 becomes predominant (4–6,9). Based on these and other observations it has been proposed that SUV39H-mediated methylation of heterochromatin is primed by an unidentified H3K9 monomethylating HMTase (59). In wild-type mammalian cells, mono- and dimethyl H3K9 are mostly found in euchromatin (4–6,9,12,32). Monomethylated forms of H3K9 and H4K20 partition together into discrete nuclear compartments that have been proposed to represent silent chromatin states, functionally different from those characterized by the di- and/or trimethylated forms (32). This organization of chromosomes into domains with distinct H3K9 methylation states has also been observed in plants (7,8,11,27). Moreover, isotope-labeling of mammalian cells to detect half lives and histone exchange rates revealed differential stability of the H3K9 methylation states: fast turnover for H3K9me1, intermediate turnover for H3K9me2 and very slow turnover for H3K9me3 (60). Thus, different degrees of H3K9 methylation may be functionally relevant. Yet, the biological significance of monomethyl H3K9 has remained unexplained because of the lack of mutants exclusively defective in this modification.

Interestingly, *Chlamydomonas* SET3p behaved as an exclusive H3K9 monomethyltranferase *in vitro* and RNAi-mediated downregulation of *SET3* significantly reduced global H3K9me1 levels *in vivo*. ChIP assays demonstrated that H3K9me1 was specifically associated with silent, multiple-copy transgenes. Moreover, the reactivation of these transgenes in the *SET3* RNAi strains correlated with the partial loss of monomethyl H3K9 from their chromatin. Somewhat surprisingly, we were unable to detect dimethyl H3K9, an abundant H3K9 modification in *Arabidopsis* (61), in whole-cell extracts or partially purified histone extracts from *Chlamydomonas*, indicating that this mark is either absent or present at very low levels in this alga. This is in agreement with an earlier report that examined bulk histone H3 modifications in *Chlamydomonas* by protein sequencing (62). On the other hand, trimethyl H3K9 was readily observable but independent of the SET3p activity. In addition, H3K9me3 was virtually absent from the silenced multiple-copy transgenes, although it was associated at low levels with the transcriptionally active *RPS3* gene. In higher plants, reports on the presence and distribution of trimethyl H3K9 have been somewhat contradictory (8,30,61) but recent observations suggest that it may be enriched in euchromatin (8,11). Conversely, monomethyl H3K9 is found preferentially in heterochromatin both in *Arabidopsis* and maize (7,8,11). Our findings in *Chlamydomonas* are also consistent with a role for H3K9me1 in indexing silent, presumably (hetero) chromatic domains, which may be typical of tandemly repeated sequences (56,57). Thus, our results, taken together, implicate SET3p as the first exclusive H3K9 monomethyltransferase and provide direct evidence that H3K9me1 may function as an epigenetic mark for repressive chromatin.

In several organisms, heterochromatin is also characterized by high levels of methylation of the underlying DNA (64,65). In plants, cytosine methylation is found predominantly at symmetric CpG and CpNpG sequences and at a lower frequency at asymmetric CpNpN sites (where N = A, T or C) (66). In *Arabidopsis*, CpG methylation appears to direct H3K9me2 to silent chromosomal regions (64,67). Conversely, several SUVH proteins seem to control the deposition of non-CpG methylation, mediated by the CMT3 chromomethylase, at distinct loci (27–29,31). Likewise, in *Neurospora*, the H3K9 HMTase Dim-5 is required for DNA methylation (23). In mammals, H3K9 methylation and CpG methylation show a complex interplay, perhaps as part of a self-reinforcing loop for repressive chromatin (53,68). The *suv39h1*/*suv39h2* double mutant cells display an altered DNA methylation profile at pericentric satellite repeats, but not at other repetitive sequences (68); whereas mouse embryonic stem cells deficient in maintenance or *de novo* DNA methyltransferases show no alteration in H3K9 methylation at several repeats (69). In green algae, cytosine methylation appears to be restricted to the CpG sequence (35,70) and a possible relationship between DNA methylation and H3K9 methylation had not been previously examined. To our surprise, we detected an increase in DNA methylation of the reactivated *RbcS2:aadA:RbcS2* transgenes in the *SET3* RNAi strains. This suggests that CpG methylation in *Chlamydomonas* is not dependent on the H3K9me1 mark. Indeed, we speculate that a reduction in H3K9 monomethylation may result in an opening of the chromatin structure and

increased accessibility of the DNA to CpG methyltransferases and/or to other factors that control DNA methylation. Transgene reactivation in this context is likely the net result of a reduction in (hetero)chromatic structure, due to suppression of SET3p activity, partly counteracted by an increase in DNA-methylation-dependent silencing.

With the present results all H3K9 methylation states have now been implicated in the establishment and/or maintenance of repressive chromatin, yet their precise roles remain unclear since their distribution in nuclear domains is species specific. Moreover, H3K9me3 has also been found associated with active genes in some species (this work and 63). The different H3K9 methylation states are in all likelihood bound by specific chromatin proteins that determine the higher order levels of chromatin organization. For instance, HETEROCHROMATIN PROTEIN1 (HP1), a key factor for heterochromatin formation in *Drosophila*, *Neurospora* and mammals, is partly localized to specific nuclear domains by preferential binding to H3K9me3 (and with lower affinity to H3K9me2); however it will not recognize chromatin characterized by H3K9me1 (65,71,72). Interestingly, in *Arabidopsis*, characterized by H3K9me1 and H3K9me2 in its heterochromatin, the putative HP1 homolog (LIKE HETEROCHROMATIN PROTEIN1) appears to be dispensable for heterochromatic silencing (28,73). Thus, there must be differences in the molecular mechanisms of recognition and interpretation of epigenetic histone modifications that ultimately produce the same functional outcome (for instance a silent heterochromatic domain) from varying methylation states in different species. Within this context, how H3K9me1 is recognized and transduced into a repressive chromatin domain, or whether it has other roles, remains to be explored. Furthermore, the cumulative evidence from multiple eukaryotes (10,59) strongly supports the notion that a combination of several histone lysine methylation marks (and probably other histone modifications as well as DNA methylation), rather than a single epigenetic mark, is required to discriminate active from inactive chromatin.

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